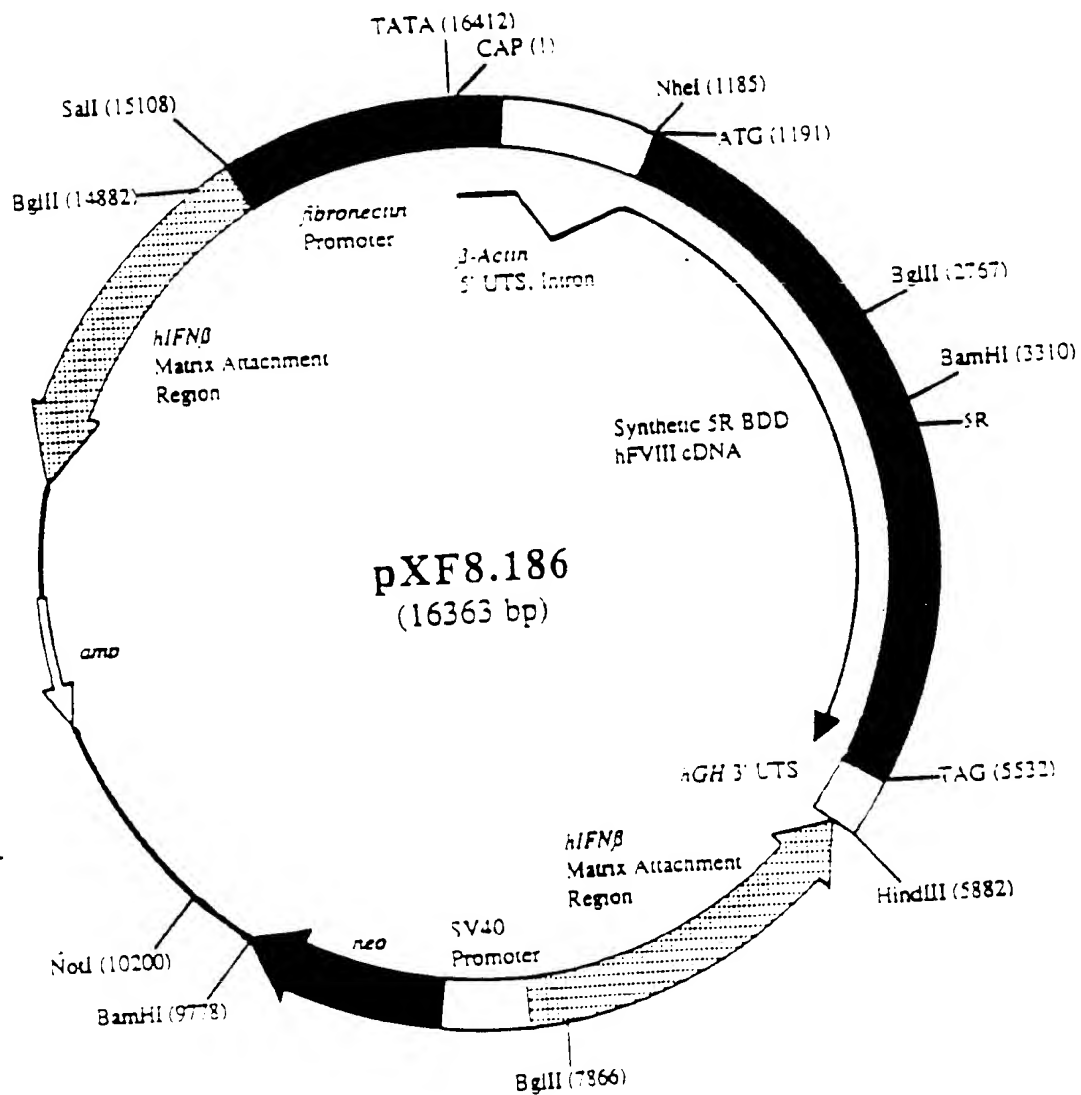


Heterogeneity of hFVIII is due to proteolysis within the B-domain

FIG. 2



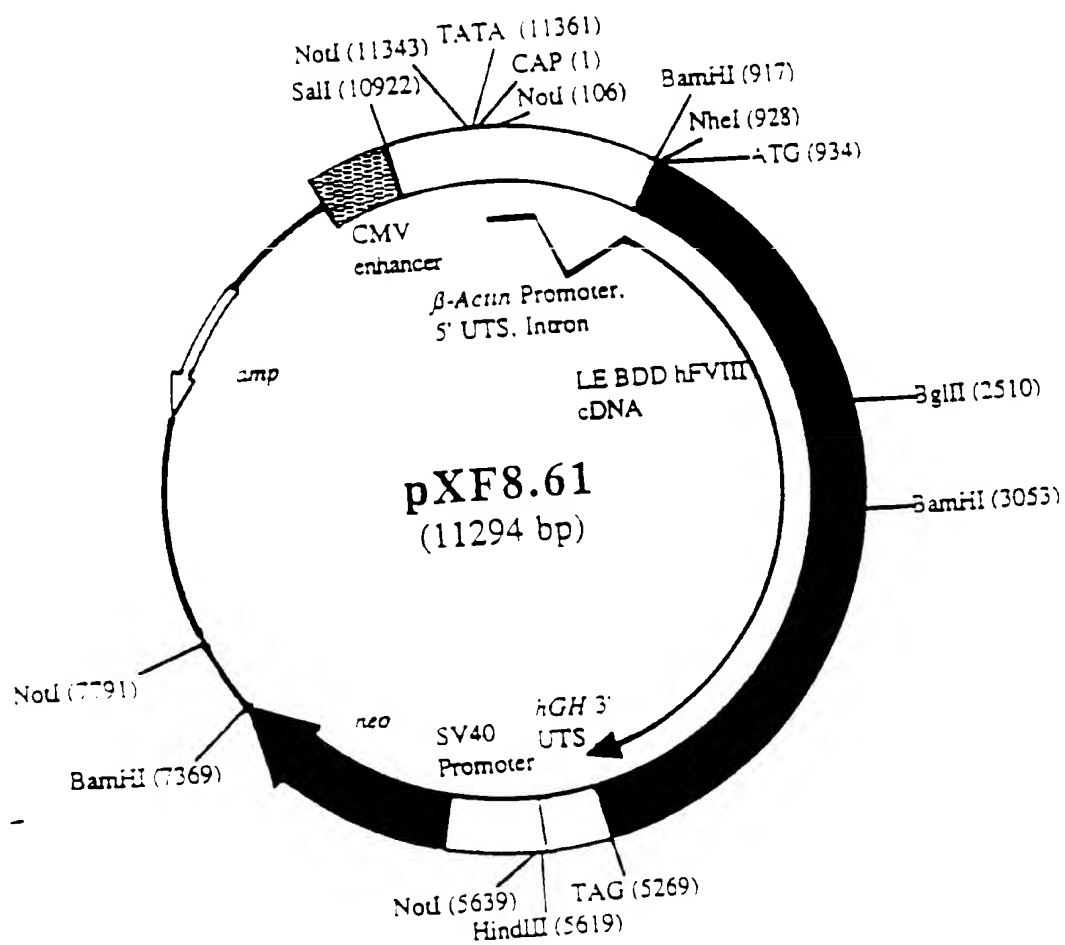


FIG. 4

Fragment A

[illegible]

FIG. 5 (1 of 14)

Fragment B

		EcoRI		ApaI			
		GTAGAATTCTGTAAGGGGCCCCACCATTCAGGCCGAGGTAGACACCGTGTGATCACCCTGAAGACATGGCCAG				AMI BI 1	
		CATCTTAAGCATCCCCGGGTGGTGAAGTCCGACTCCACATGTGTGGACACCATTAATGGGACTTCTTGTACCGGTG					
		AMI Br3					
		3' OH 5' P					
		CCACCCCGTGAGC TGTGACGCCGTGGGCGTGAGCTACTG GAAGGCCAGGAGGCGCCGAGTAGACGACCA					
		GGTGGGGCACTCG GACGTGCTTATTTGCACTCGATGAC CTTCGGGTGCTGCCGGCTCATTCCTGTGCTCTP					
		5' P 3' OH					
		AMI BI2					
		CCAGCCAGCGCGAGAAGAGGACGACAAAGGTGTTCCCGG TCGGACGACAGACCTAAGTGTGGCAGTG CTGAAG					
		GGTCGGTCCGCTCTTCTCTCTGCTGTTCACACAGGGGGCG GCCGTGGTGTGATGACACCGCTCCAC GACTTTC					
		5' P 3' OH					
		AMI BI3					
		PmII					
		HindIII					
		GAGAACGGCCCCCATGGCCAGCGACCCCTGTGCTGACCTACGTAAGTAAGTACCTGAGCCACGTGCTACAAAGCTTTAC					
		CTCTTTGGCCGGGTACCGCGTGGCGTGGAGACACGGAAGTGGATGTGATGACTCGGTGGACGATGTTGGAATG					
		AMI Br1					

FIG. 5 (2 of 14)

AMICI

AM1Cf2

AM1Cr2

5'-p-3'-OH

AM1Cr1

FIG. 5 (3 of 14)

Fragment D

EcoRI PmlI
 GTAGATTCGTAGCAGCGTATCGGCATGGGCAACACCCCGAGGTGCACAGCATCTTCCCTGGAGGGCCACAC¹CTTCTGTGTCGCCAACCACCG
 CATCTTAAGATCGTGCACCTAGCCGTACCCCGTGGTGGGGCTCCACGCTGTCTAGAAATGACCTTCCCGGTGTG GAAGAACCAACGCTTGGTGGG
 5' P 3' OH
 AM1D11
 AM1D12
 3' OH 5' P
 CCAGGC¹CAGCCTGAGATCAGCCCCCATCACCCTTCTGACCGCCAGACCCCTGTGATGGACCTGGGCCAGTTCTCTGTCTGT¹CTGCCACATCA
 GGTCCG¹GTCGAGCTCTAGTCGGGGTAGTGGAAAGACTGGCGGGTCTGGACGACTACCTGTGATCTCTCAAGAGACGACAA¹GACGGTGTACT
 5' P 3' OH
 AM1D13
 3' OH 5' P
 GCAGCCACCGAC¹GACGCATGGAGGCCCTACCTGTAAGTGGACAGCTGCCCGAGAGAGGCCCGACGCTGCCGATGAAGAACAAAGAGAGG¹TCC
 CTTCCGCTGTCTGTG¹CTGCCGTACCTCCGGATGCACCTTCCACCTGTGACGCGGGCTCTCCGGATGACGGCGTACTTCTTGTGTCTCTCC¹TCC
 5' P 3' OH
 AM1D12
 3' OH 5' P
 GAGGACTACGACGACGACCTGAC¹CGACAGCGAGATGACCTGTGGCTTGCAGACGACACACACAGCCCCAGCTTCATCCAGATCTTACGGAT
 CTTCTGATGCTGTCTGTGACTG¹GCTGTCTCTTACCTGCACCAACGGAAGCTGTGCTGTGTGTGGGGTGCAGTAGTCTTAAAGATGCTTA
 5' P 3' OH
 AM1D14
 BglII BamHI
 CCTACAAGCTTTAC
 GATGTGTGGAAATG

Fragment E

EcoRI BamHI AM1E11
 GTAGATTCGTAGGATCCGACGCGTGGCCAGAA3CACCCCAAGACCTGGGTTCATCATGCGCCGAGAGAGAGACTGGACTACGC
 CATCTTAAAGCATCCCTAGGCGTCGCACCCGGTTCCTTCGTGGGGTTCTGATGCCCTCTCTGATCTTGATTCG

3' OH 5' P
 CCCCCCTG TATCTGCCCCCGACGACCGCAG CTACAAGAGCCAGTACCTGAACAACGGCCCCCAGCGCATTCACAGTACAGAGGT
 CAGGAGC CACGACCGGGGGCTGCTGGCGTC CATGTTCTCGGTATGACTTGTGCCGGATTCGCGGCGTACCGCGTTCATGTTCTTCA
 5' P 3' OH AM1E3

3' OH 5' P ApaI
 CCGCATCCTGGGCCCCCTGCTGACGGGA
 GCGCTTCATGGCCTACACCGACGAGACCTTCAAGACCC TCGAGGCCATCCAGACGAGAG CCGCATCCTGGGCCCCCTGCTGACGGGA
 CCGTCAAGTACCGGATGTGGCTGCTCTGGAAGTTCTGGG CCGTCCGTAAGTCGCTCTC CCGTACGACCCGGGACGACATGCTCT
 3' OH 5' P AM1E12
 GGTGGCGACACCCCTGCTGATCATCTTCAAGAACGAGCCAGCCGCGCCCTACACATCTAAC TCCACGGCATACCGACGTCGC CCCC
 CACCCCTGTGGGACGACTAGTAAGTTCTTGTCCCGTCGCGGGGATGTTGTAGATCG GGTGCCGTAGTGGCTGCACCCG

3' OH 5' P BglIII HindIII
 GTACAGCCCGCCGCTGCCCCAAGGGCGTGAAGCACCTGAAGACTTCCCATCTGCCCCGAGATCTCTACAGCTTAC
 CATCTTCGCGCGCAACGGCTTCCCGCACTTCTGTGACTTCTGAAAGGGTAGACGGGCTGCTTGAAGATGTTCCGAATG

AM1E2 AM1E14 AM1E1
 AM1E13

FIG. 5 (5 of 14)

AM1F1

HindIII KpnI AM1 F11
 GTAAGCTTGTAGGTACCACTGGCGTTTCCTGACACAGCTGAACAGATCAGCTTGC TCTTGTGGCTCATGATCTGGTTGCC
 TAAATTCGACATCCATGCTGCAGCGCCAGAGCAGCTGTGCGACTTGTCTTAGTCTACG TGNACAGCGAGTACTAGACCAACGAT
 AM1 F13 AM1 F12
 5' P 3' OH

AM1 Fr3

AM1F12

3:01:51 P

OH 5' P
 1 1
 6 CGGTGCTCAGCGCTCTCTGTAGCAGATTCAGCAGGGGGGCGATCAGGCGCTGGCCAGGTCCGCTCCATGTTAC TGAACCTG
 C GCGACCAAGGTGCGAGAGAACATCTGTTAGTCTGTCCTCCCGCTAGTCCGGCGACCGTTCACGCGAGGTACAAAGTGT CTTCGAC
 C GCGACCAAGGTGCGAGAGAACATCTGTTAGTCTGTCCTCCCGCTAGTCCGGCGACCGTTCACGCGAGGTACAAAGTGT CTTCGAC
 AM1F12
 AM1F12
 5' P 3' OH

AMiFr2

AM1F13

B9111

3:04.51 p

3' OH 5' P

CCTGAGTAGCGGGTCAG¹ CAGCGGGGTCCTCTTCTTGGGGCEGTCCACGGTCACCGTTCACCTGTACTGAGAATCTCTAAG
GACATTCATCGGCCAGTC² CGTCGCCCCCTACCAAGAACCCACCCTCCGGCAGAGGTGCACATCTCTAGGTGACATGAATCTCTTAAGAAATAT

AM1 Fr1

AM1Fr1

Eqn 11

CGAATTCCTAC
CTTAAAGATG

FIG. 5 (6 of 14)

Fragment G

EcoRI KpnI
 GTAGAAATTCGTAGGGTACTGACCGAGAACATCCAGGCTTCTCCCAACCCCGCGCGGTGCAGCTGGAGAGACCCCGAGTTCCAGGCCAG
 TATCTTAAACATCCCATGGACTGGCTTCCTTCTAGAGATTCGCGAAGGACCGGGTTGGGGCGCGCACTTCGACCTCCTGGGGCTTACCTTCGGCTC
 AMIGr1
 3' OH 5' P
 CAACATTCATGCACAGCATCAACGGGCTAC GTGTTCGACAGCCTGCAGCTGAGCGTGTGCTGCACAGAGTGGCCCTACTGGTACATCCTGAG
 GTTGTATGTACGTGTGTAGTTGCCGATG TACAGCTGTGGAAGTCACTCCCAACCGGATCTTCACCGGATGACCATGTAGGACTC
 5' P 3' OH
 CATCGGGCGCCAGACCGACTTCTGAGCGTGTCTTTCAGC TGGCTACACCTTCAAGCACAAGATG GTGTACGAGGACACCCCTGACCTGT
 CTAGCCCGCGGCTCTGGCTGAAGACTCGGACATGAGATCG TCGATGTGAAGTTCTGTCTTAC CACATGCTCTCTGTGGGACTTGGGAC
 5' P 3' OH
 AMIGr3
 BamHI HindIII
 CCCCCTCAGCGGAGAGACCGTGTCTCATGAGCATGAGAACCCCGCGCTGTGATCCCTACACAGCTTTAC
 GAGGAAAGTCCGCGCTCTGGCACAAATACCTTCTTGGGGCCGGACACCTTAGGATGTGTTCGAATG
 AMIGr1
 AMIGr2
 3' OH 5' P
 AMIGr12

FIG. 5 (7 of 14)

Fragment H

[illegible]

FIG. 5 (8 of 14)

Fragment 1

EcoRI PstI
 CTAGAAATTCGTAGCAGCGTGTGCGCAACCGCGCCAGACCTGACAGCGGTGCGGCCAGTTCAGAAGGTGTGTCAGAGATTACCGAGCGGACCTCTTACCCAA
 CATCTTAAAGCATGCTGCACGACGCGGTTGGCGGGTCTGTGTGTCGACGCGGGTCAAGTCTTCCACCACACAGGTCTCAGTGGCTGCGGTG 5' P 3' OH

3' OH 5' P
 CCCCCTGTACCGGC GCGGAGCTGAACGAGCACCCTGGGCGCTGCTGGGCCCCCTACATCCGCGCGAGGTGAGACGACACATCATGTGTGACCGGTGACGAGTTCG
 GATTAACATGCGGCTCCGCTGTACCTTCTCTGTGACCCCGAGCTAACCCGGGATGTAGCGCGGCTCCACCTCTCTTTTGTAGTACCACTGGCACTGTCTTCAAGT 5' P

AM11r3 AM11l2 AM11l3
 AM11l3 AM11l2 AM11l3

3' OH 5' P
 CTGTCTTCACGACATCTTGCAG GAGACCAAGAGCTGTGATCTTACCGAGACATGAGCGCACTGCGCGCGCCCTGCAACATCCAGATGAGGAGACCTCTG
 GATTAACATGCGGCTCCGCTGTACCTTCTCTGTGACCCCGAGCTAACCCGGGATGTAGCGCGGCTCCACCTCTCTTTTGTAGTACCACTGGCACTGTCTTCAAGT 5' P 3' OH

AM11l2 AM11l4 AM11l3
 AM11l2 AM11l4 AM11l3

3' OH 5' P
 TTCAAGGAGACTACCGCTTCCAG CCAATCAAGCGCTACATCATGACACCCCTGCCCCGCTGTGATGCGCCAGAGCAGCGCATCCGCTGTACCCCTAC
 AATCTTCTTGTGATGCGGAGGTGC GGTAGTTCGGATTCATGTAACCTGTGGACGGCGCGGACCACTACATGATGATCTGCTGTGCGGTAGGCGGACCATTTGGAT

AM11l1 AM11l4 AM11l3
 AM11l1 AM11l4 AM11l3

KpnI
 GCTTTAC
 CGAATATG

FIG. 5 (9 of 14)

AMI J11
 EcoRI **Bst**II
 GTGAATTCGTAGGCTGACCTTCGCAACCAAGCCAGCCGCCCTACAGCTTCTACAGCAGCAGCCTGATCAGCTACGAGGAGGACCAGCC
 CTATCTTAAGCATCCCACTGGAAGGCTTGTGTCCGGTCCGGGGGATGTGGAAGATGTGCTGGACTAGTCGATGCTCTTCTGTGCTCCG
AMI J13
 AMI J13 **Eag**I **Bst**II **Hind**III
 GTGGTCCACACCAACACACCCTGAACCCCGCCACAGCGCCGCCAGTGACCTACAAAGCTTAC
 CTATACGGTGTGTGTGGGACTTGGGGCGGATGCCGGCGGTCCACTGGGATGTCGAATTC
AMI J12
 AMI J12
 AGGTTCCCTGAGCCCCCGCAAGACTTC GTGAAGCCCCCAAGAGACCAAGACCTTCTCTGGAAGTGCAGCACCACATGGCCCCCAGCA
 TCC GCGGCTCGGGCGCTCTTGAAAGCTACCTTGGGCTTCTCTGTGTGATGAAAGACCTTCCACGTCGTGCTGTACCTGAGGTTGCTT
 5' P 3' OH
 3' OH 5' P
AMI J14
 GAGCAGATTCGACTGCAAGCGCTGGGCTTACTTTCAGCTGACGTGACCTGAGAAAGAC GTGCACAGCGGCTGATCGGCCCTGCTG
 CCTTCTCAAGCTGACGTTCCCGACCCCGATGTAGTC GTGACACTGACCTCTTCTCTCTACGTGTGCGCGGACTAGCCCGGAGAGGAC
 5' P 3' OH
 3' OH 5' P

FIG. 5 (10 of 14)

[illegible]

FIG. 5 (11 of 14)

Fragment L

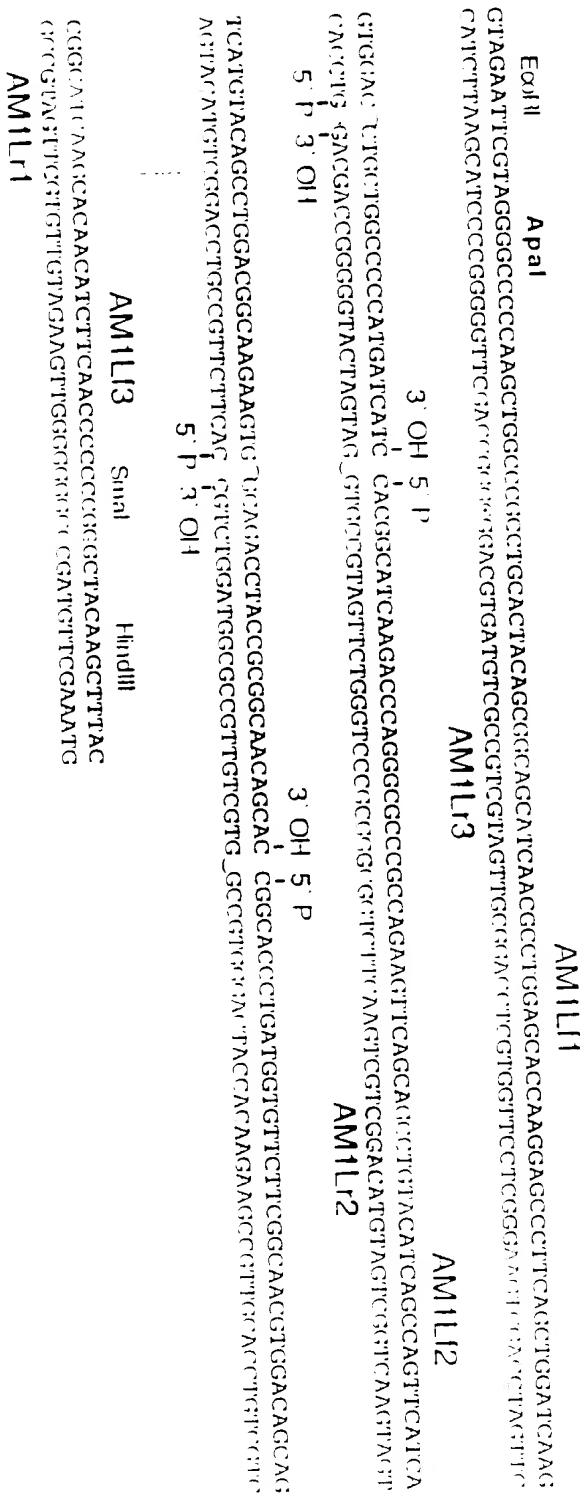


FIG. 5 (12 of 14)

EcoRI
 5' P 3' OH
 GAGGATTCGATGATATCATCCGCCGTACATCCGCCCTGCACCCACCACCTACAGACATCCGACAGCACCCCTGGCATGAGCTGATGGG
 CATCTTAAGCATCTCTATGATGACGGGGCATTTGAGCCGACCGTGGGGTGGTGTATGTCTGTAAGCGTCTGGAGACGGGTATCTTCTGATACCTC
 AM1M1
 AM1M1M1
 AM1M1M2
 AM1M1M3
 BstEII
 HindIII
 AAGAGTGGCTGCAGGTGGACTTCCAGAAGACCATGAAGTGACCCCTACACAGCTTTAC
 TCCCTACCGACGTCCACCTGAAAGGTCTTCTGCTACTTCCACTGGGATGTTGAAATG
 AM1M1M1
 AM1M1M2
 AM1M1M3
 AM1M1M4
 AM1M1M5
 AM1M1M6
 AM1M1M7
 AM1M1M8
 AM1M1M9
 AM1M1M10
 AM1M1M11
 AM1M1M12
 AM1M1M13
 AM1M1M14
 AM1M1M15
 AM1M1M16
 AM1M1M17
 AM1M1M18
 AM1M1M19
 AM1M1M20
 AM1M1M21
 AM1M1M22
 AM1M1M23
 AM1M1M24
 AM1M1M25
 AM1M1M26
 AM1M1M27
 AM1M1M28
 AM1M1M29
 AM1M1M30
 AM1M1M31
 AM1M1M32
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 AM1M1M38
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 AM1M1M88
 AM1M1M89
 AM1M1M90
 AM1M1M91
 AM1M1M92
 AM1M1M93
 AM1M1M94
 AM1M1M95
 AM1M1M96
 AM1M1M97
 AM1M1M98
 AM1M1M99
 AM1M1M100

Fragment N

[illegible]

FIG. 5 (14 of 14)

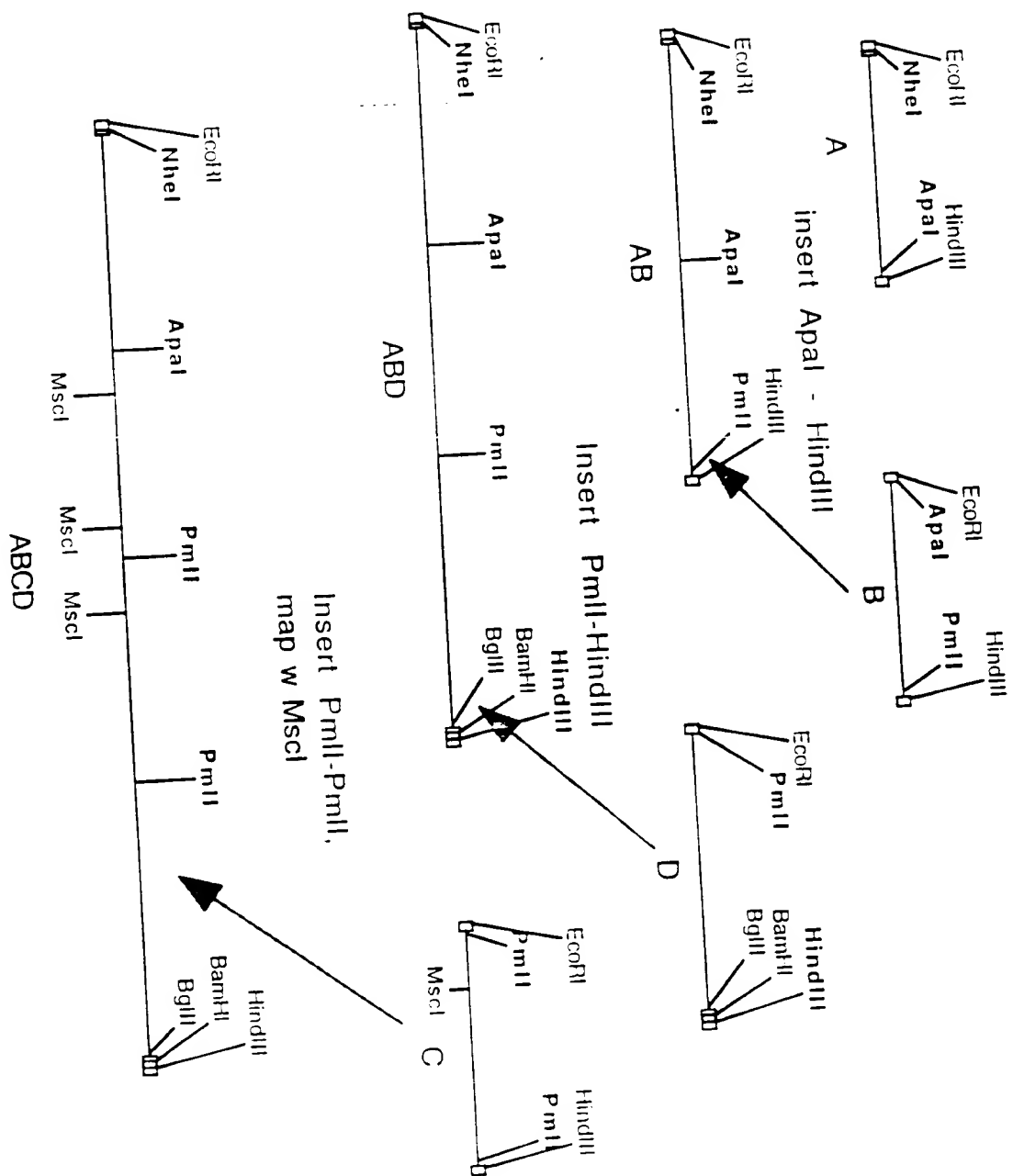


FIG. 6 (1 of 5)

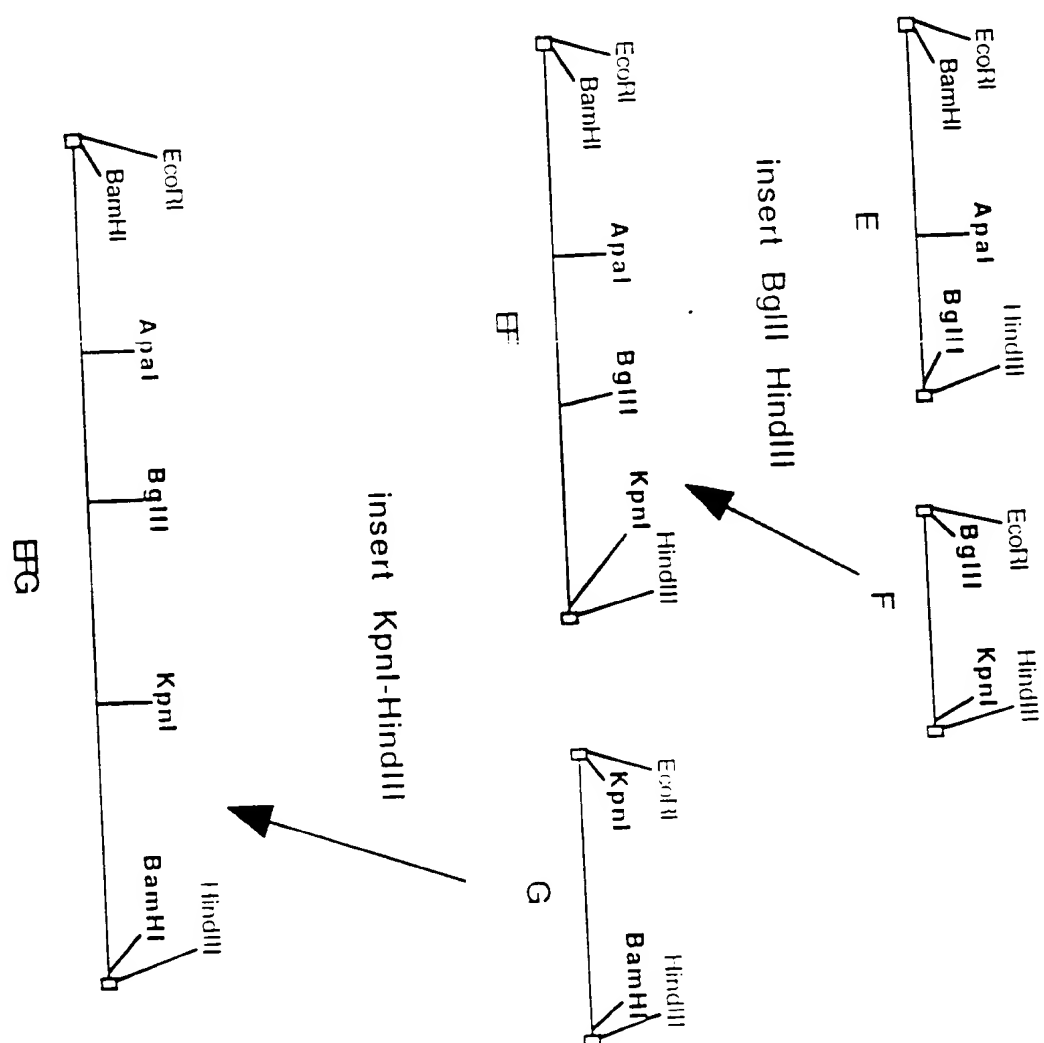


FIG. 6 (2 of 5)

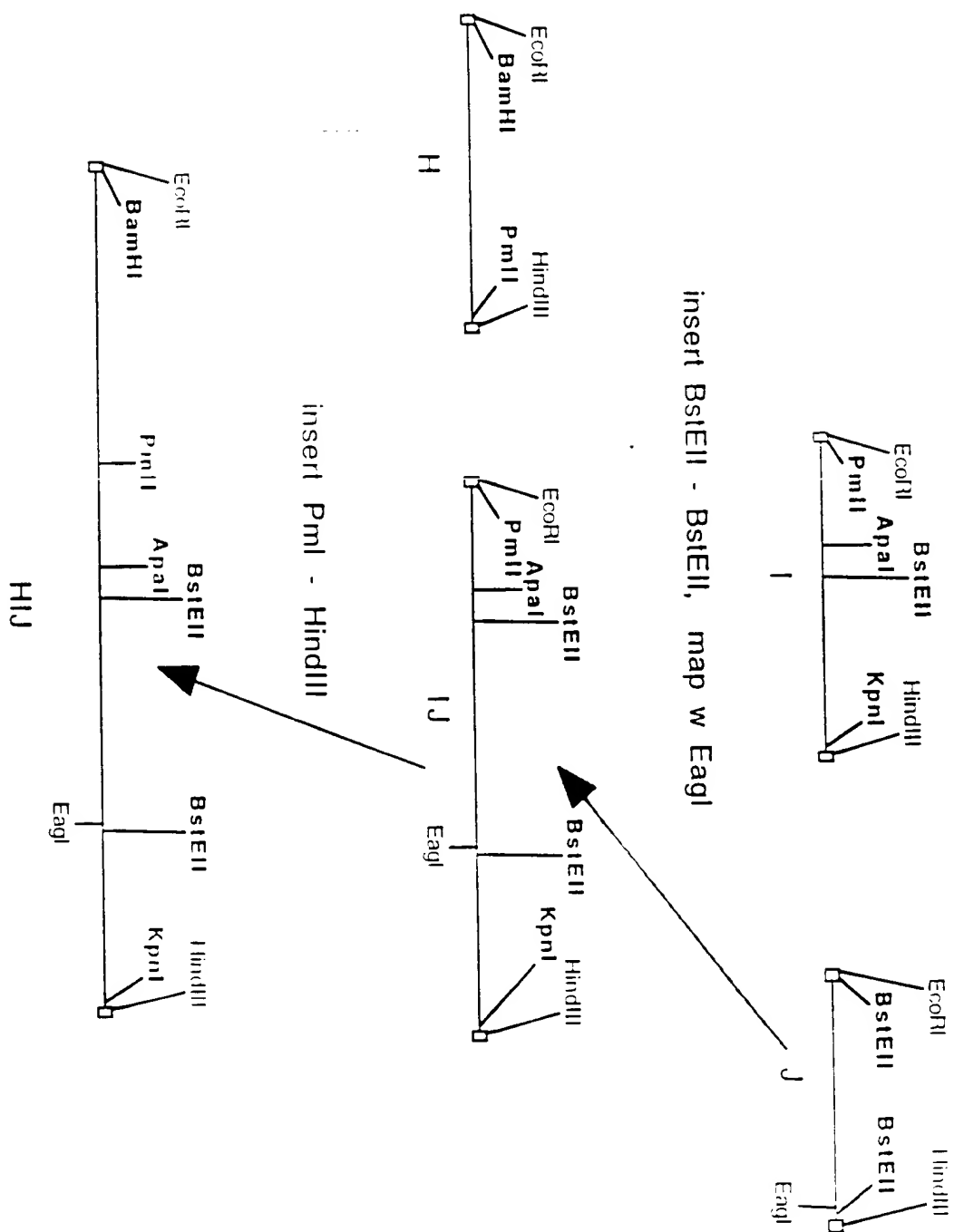


FIG. 6 (3 of 5)

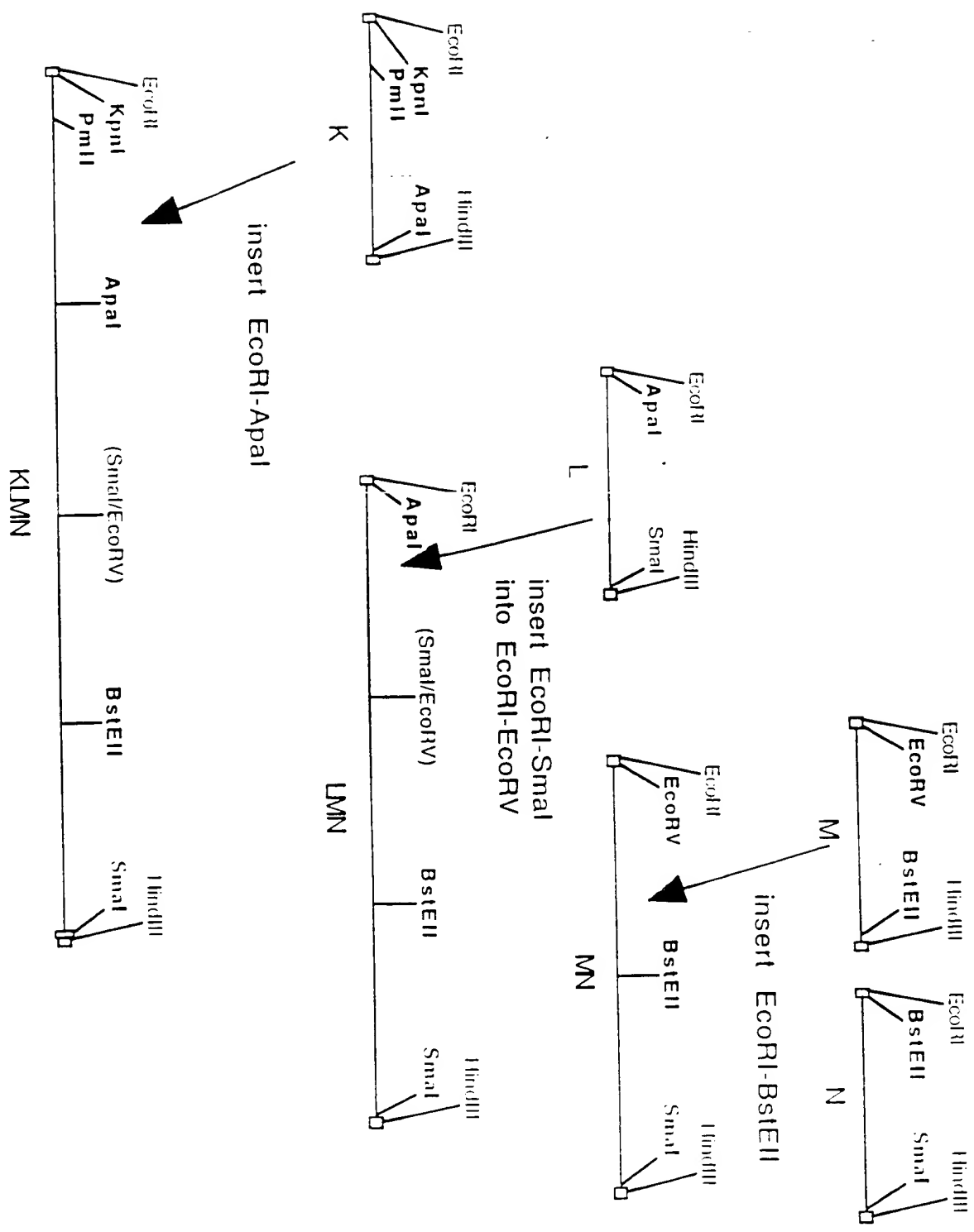


FIG. 6 (4 of 5)

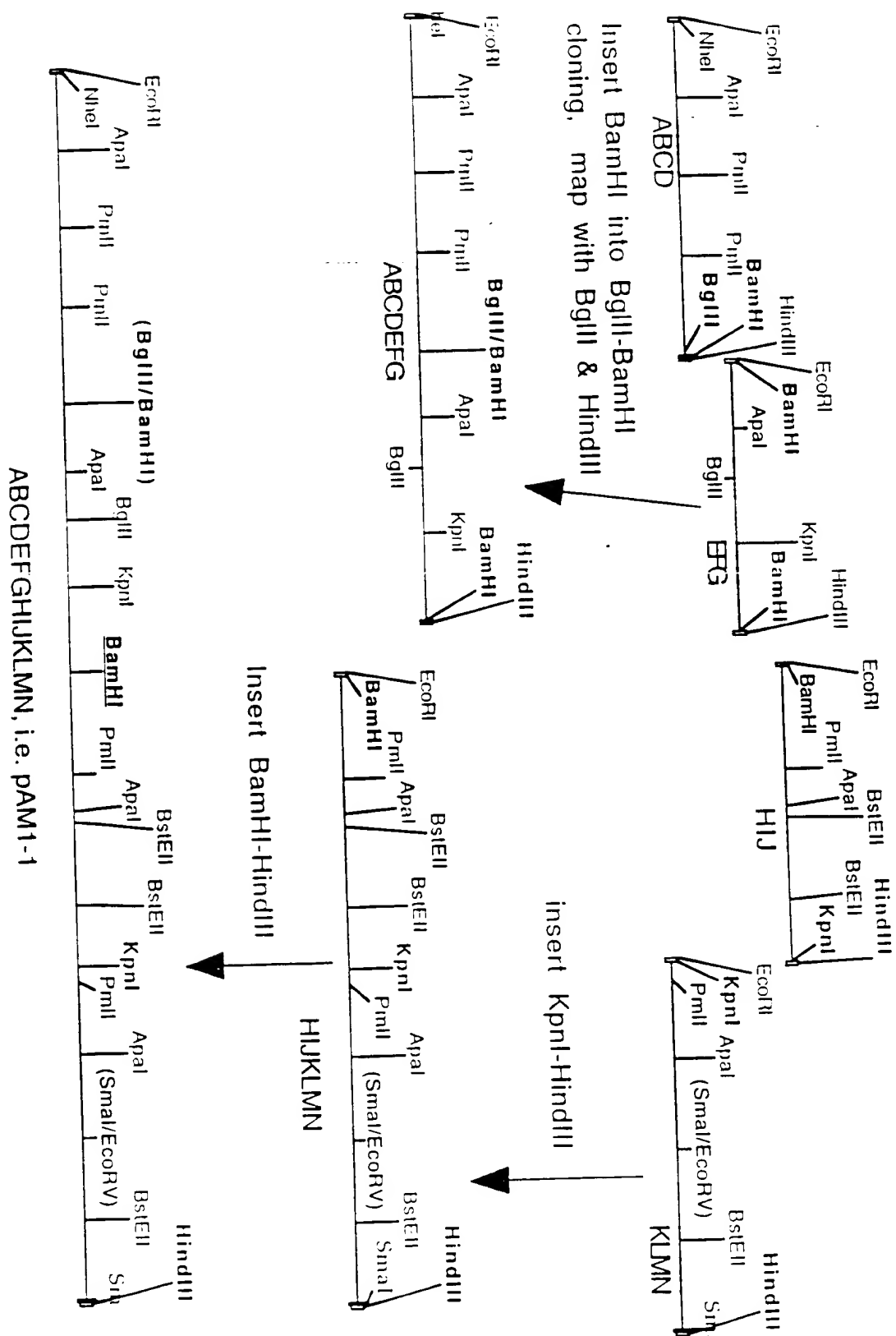


FIG. 6 (5 of 5)

EcoRI NheI

1 TAGAATTCGCTAGGCTAGCATCCAGATCCAGCTCAGCACCTTCTTCTCTGTGCCTGCTGCGCTTCTGCTTC
1▶ MetGlnIleGluLeuSerThrCysPhePheLeuCysLeuLeuArgPheCysPhe

73 AGCGCCACCCGCCGCTACTACCTGGCGCCCGTGAGCTCAGCTGGGACTACATGCAGAGCGACCTGGGCGAG
19▶ SerAlaThrArgArgTyrTyrLeuGlyAlaValGluLeuSerTrpAspTyrMetGlnSerAspLeuGlyGlu

145 CTGCCCCGTGGACGCCCCGCTTCCCCCCCCCCGCTGCCCAAGAGCTTCCCCTTCAACACCAGCGTGGTGTACAAG
43▶ LeuProValAspAlaArgPheProProArgValProLysSerPheProPheAsnThrSerValValTyrLys

217 AAGACCCTGTTTCGTGGAGTTCACCGACCACCTGTTCAACATCGCCAAAGCCCCGCCCCCCTGGATGGGCGCTG
67▶ LysThrLeuPheValGluPheThrAspHisLeuPheAsnIleAlaLysProArgProProTrpMetGlyLeu

Apal MscI

289 CTGGGCCCCACCATCCAGGCCGAGGTGTACGACACCGTGGTGATCACCTGAAGAACATGGCCAGCCACCCC
91▶ LeuGlyProThrIleGlnAlaGluValTyrAspThrValValIleThrLeuLysAsnMetAlaSerHisPro

361 GTGAGCCTGCACGCCGTGGGCGTGAGCTACTGGAAGGCCAGCGAGGGCGCCGAGTACGACGACCAGACCAGC
115▶ ValSerLeuHisAlaValGlyValSerTyrTrpLysAlaSerGluGlyAlaGluTyrAspAspGlnThrSer

433 CAGCGCGAGAAGGAGGACGACAAGGTGTTCCCCGGCGGCAGCCACACCTACGTGTGGCAGGTGCTGAAGGAG
139▶ GlnArgGluLysGluAspAspLysValPheProGlyGlySerHisThrTyrValTrpGlnValLeuLysGlu

MscI PmlI

505 AACGGCCCCATGGCCAGCGACCCCCCTGTGCCTGACCTACAGCTACCTGAGCCACGTGGACCTEGTGAAGGAC
163▶ AsnGlyProMetAlaSerAspProLeuCysLeuThrTyrSerTyrLeuSerHisValAspLeuValLysAsp

MscI

577 CTGAACAGCGGCCCTGATCGGCGCCCTGCTGGTGTGCCGCGAGGGCAGCCTGGCCAAGGAGAAGACCCAGACC
187▶ LeuAsnSerGlyLeuIleGlyAlaLeuLeuValCysArgGluGlySerLeuAlaLysGluLysThrGlnThr

649 CTGCACAAGTTCATCCTGCTGTTCCGCGTGTTCGACGAGGGCAAGAGCTGGCACAGCGAGACCAAGAACAGC
211▶ LeuHisLysPheIleLeuLeuPheAlaValPheAspGluGlyLysSerTrpHisSerGluThrLysAsnSer

721 CTGATGCAGGACCGCGACGCCGCCAGCGCCCGCGCTGGCCCAAGATGCACACCGTGAACGGCTACGTGAAC
235▶ LeuMetGlnAspArgAspAlaAlaSerAlaArgAlaTrpProLysMetHisThrValAsnGlyTyrValAsn

PmlI

793 CGCAGCCTGCCCCGGCCTGATCGGCTGCCACCGCAAGAGCGTGTACTGGCACGTGATCGGCATGGGCACCACC
259▶ ArgSerLeuProGlyLeuIleGlyCysHisArgLysSerValTyrTrpHisValIleGlyMetGlyThrThr

865 CCCGAGGTGCACAGCATCTTCTGGAGGGCCACACCTTCTGGTGGCGCAACCACCGCCAGGCCAGCCTGGAG
283▶ ProGluValHisSerIlePheLeuGluGlyHisThrPheLeuValArgAsnHisArgGlnAlaSerLeuGlu

937 ATCAGCCCCATCACCTTCTGACCGCCCCAGACCCTGCTGATGGACCTGGGCCAGTTCCTGCTGTTCTGCCAC
307▶ IleSerProIleThrPheLeuThrAlaGlnThrLeuLeuMetAspLeuGlyGlnPheLeuLeuPheCysHis

1009 ATCAGCAGCCACCAGCACCGGCGATGGAGGCCTACGTGAAGGTGGACAGCTGCCCCGAGGAGCCCCAGCTG
331▶ IleSerSerHisGlnHisAspGlyMetGluAlaTyrValLysValAspSerCysProGluGluProGlnLeu

1081 CGCATGAAGAACAACGAGGAGGCCGAGGACTACGACGACGACCTGACCGACAGCGAGATGGACGTGGTGGCG
355▶ ArgMetLysAsnAsnGluGluAlaGluAspTyrAspAspAspLeuThrAspSerGluMetAspValValArg

(BglII/BamHI)

1153 TTCGACGACGACAACAGCCCCAGCTTCATCCAGATCCCGACGCTGGCCAAGAAGCACCCCCAAGACCTGGGTG
379▶ PheAspAspAspAsnSerProSerPheIleGlnIleArgSerValAlaLysLysHisProLysThrTrpVal

1225 CACTACATCGCCGCGGAGGAGGAGGACTCGGACTACGCCCCCTGGTGTCTGGCCCCGACGACCGCAGCTAC
403▶ HisTyrIleAlaAlaGluGluGluAspTrpAspTyrAlaProLeuValLeuAlaProAspAspArgSerTyr

EagI

1297 AAGAGCCAGTACCTGAACAACGGCCCCCAGCCCATCGGCCCAAGTACAAGAAGGTGCGCTTCATGGCCTAC
427▶ LysSerGlnTyrLeuAsnAsnGlyProGlnArgIleGlyArgLysTyrLysLysValArgPheMetAlaTyr

Apal

1369 ACCGACGAGACCTTCAAGACCTGGGAGGCCATCCAGCACGAGAGCGGCATCCTGGGCCCCCTGCTGTACGGC
451▶ ThrAspGluThrPheLysThrArgGluAlaIleGlnHisGluSerGlyIleLeuGlyProLeuLeuTyrGly

1441 CAGGTGGGGGACACCCCTGCTGATCATCTTCAAGAACCAGGCCAGCCGCCCCCTACAACATCTACCCCCACGGC
 475▶ GluValGlyAspThrLeuLeuIleIlePheLysAsnGlnAlaSerArgProTyrAsnIleTyrProHisGly
 1513 ATCACCAGCGTGCGCCCCCTGTACAGCCCGCCCTGCCCAAGGGCGTGAAGCACCTGAAGGACTTCCCCATC
 499▶ IleThrAspValArgProLeuTyrSerArgArgLeuProLysGlyValLysHisLeuLysAspPheProIle

BglII

1585 CTGCCCCGGCGAGATCTTCAAGTACAAGTGGACCGTGACCGTGGAGGACGGCCCCACCAAGAGCGACCCCGCG
 523▶ LeuProGlyGluIlePheLysTyrLysTrpThrValThrValGluAspGlyProThrLysSerAspProArg
 1657 TGCCTGACCCGCTACTACAGCAGCTTCGTGAACATGGAGCGCGACCTGGCCAGCGGCCTGATCGGCCCCCTG
 547▶ CysLeuThrArgTyrTyrSerSerPheValAsnMetGluArgAspLeuAlaSerGlyLeuIleGlyProLeu
 1729 CTGATCTGCTACAAGGAGAGCGTGGACCAGCGCGGCAACCAGATCATGAGCGACAAGCGCAACGTGATCCTG
 571▶ LeuIleCysTyrLysGluSerValAspGlnArgGlyAsnGlnIleMetSerAspLysArgAsnValIleLeu

KpnI

1801 TTCAGCGTGTTCGACGAGAACCAGCGCTGGTACCTGACCGAGAACATCCAGCGCTTCCTGCCCAACCCCGCC
 595▶ PheSerValPheAspGluAsnArgSerTrpTyrLeuThrGluAsnIleGlnArgPheLeuProAsnProAla
 1873 GGCGTGACGCTGGAGGACCCGAGTTCAGGCCAGCAACATCATGCACAGCATCAACGGCTACGTGTTTCGAC
 619▶ GlyValGlnLeuGluAspProGluPheGlnAlaSerAsnIleMetHisSerIleAsnGlyTyrValPheAsp
 1945 AGCCTGCAGCTGAGCGTGTGCCTGCACGAGGTGGCCTACTGGTACATCCTGAGCATCGGCGCCCGAGCCGAC
 643▶ SerLeuGlnLeuSerValCysLeuHisGluValAlaTyrTrpTyrIleLeuSerIleGlyAlaGlnThrAsp
 2017 TTCCTGAGCGTGTTCCTCAGCGGCTACACCTTCAAGCACAAGATGGTGTACGAGGACACCCTGACCCTGTTC
 667▶ PheLeuSerValPhePheSerGlyTyrThrPheLysHisLysMetValTyrGluAspThrLeuThrLeuPhe

BamHI

2089 CCCTTCAGCGGCGAGACCGTGTTCATGAGCATGGAGAACCCCGGCCTGTGGATCCTGGGCTGCCACAACAGC
 691▶ ProPheSerGlyGluThrValPheMetSerMetGluAsnProGlyLeuTrpIleLeuGlyCysHisAsnSer
 2161 GACTTCCGCAACCCGCGCATGACCGCCCTGCTGAAGGTGAGCAGCTGCGACAAGAACCCGCGGACTACTAC
 715▶ AspPheArgAsnArgGlyMetThrAlaLeuLeuLysValSerSerCysAspLysAsnThrGlyAspTyrTyr
 2233 GAGGACAGCTACGAGGACATCAGCGCCTACCTGCTGAGCAAGAACAACGCCATCGAGCCCCCGCTGGAGGAG
 739▶ GluAspSerTyrGluAspIleSerAlaTyrLeuLeuSerLysAsnAsnAlaIleGluProArgLeuGluGlu

BstXI

2305 ATCACC CGCACCACCCCTGCAGAGCGACCAGGAGGAGATCGACTACGACGACACCATCAGCGTGGAGATGAAG
 763▶ IleThrArgThrThrLeuGlnSerAspGlnGluGluIleAspTyrAspAspThrIleSerValGluMetLys
 2377 AAGGAGGACTTCGACATCTACGACGAGGACGAGAACCAGAGCCCCCGCAGCTTCCAGAAGAAGACCCGCCAC
 787▶ LysGluAspPheAspIleTyrAspGluAspGluAsnGlnSerProArgSerPheGlnLysLysThrArgHis

PmlI

2449 TACTTCATCGCCCGCGTGGAGCGCCTGTGGGACTACGGCATGAGCAGCAGCCCCCACGTGCTGCGCAACCGC
 811▶ TyrPheIleAlaAlaValGluArgLeuTrpAspTyrGlyMetSerSerSerProHisValLeuArgAsnArg
 2521 GCCCAGAGCGGCAGCGTGCCCCAGTTCAAGAAGGTGGTGTTCAGGAGTTCACCGACGGCAGCTTCACCCAG
 835▶ AlaGlnSerGlySerValProGlnPheLysLysValValPheGlnGluPheThrAspGlySerPheThrGln

Apal

2593 CCCCCTGTACCGCGCGGAGCTGAAGCAGCACCTGGGCCTGCTGGGCCCCCTACATCCGCGCCGAGGTGGAGGAC
 859▶ ProLeuTyrArgGlyGluLeuAsnGluHisLeuGlyLeuLeuGlyProTyrIleArgAlaGluValGluAsp

BstEII

2665 AACATCATGGTGACCTTCCGCAACCAGGCCAGCCGCCCCCTACAGCTTCTACAGCAGCCTGATCAGCTACGAG
 883▶ AsnIleMetValThrPheArgAsnGlnAlaSerArgProTyrSerPheTyrSerSerLeuIleSerTyrGlu
 2737 GAGGACCGAGCGCCAGGGCGCCGAGCCCCCAAGAAGTTCGTGAAGCCCGACGAGACCAAGACCTACTTCTGG
 907▶ GluAspGlnArgGlnGlyAlaGluProArgLysAsnPheValLysProAsnGluThrLysThrTyrPheTrp
 2809 AAGGTGCAGCACCACATGCCCCCACCAGGACGAGTTCGACTGCAAGGCCTGGGCCTACTTCAGCGACGTC

1381 AACCTCGAGAAGGACGTGCACAGCGGCGCTGATCGGGCCCCCTGCTGGTGTGCCACACCAACACCCTGAACCCC
 955▶ AspLeuGluLysAspValHisSerGlyLeuIleGlyProLeuLeuValCysHisThrAsnThrLeuAsnPro

EagI BstEII

1953 CCCCACGGCGCCAGGTGACCGTGCAGGAGTTCGGCCCTGTTCTTCACCATCTTCGACGAGACCAAGAGCTGG
 979▶ AlaHisGlyArgGlnValThrValGlnGluPheAlaLeuPhePheThrIlePheAspGluThrLysSerTrp
 3025 TACTTCACCGAGAACATGGAGCGCACTGCCGCGCCCCCTGCAACATCCAGATGGAGGACCCCCACCTTCAAG
 1003▶ TyrPheThrGluAsnMetGluArgAsnCysArgAlaProCysAsnIleGlnMetGluAspProThrPheLys
 3097 GAGAACTACCGCTTCCACGCCATCAACGGCTACATCATGGACACCCTGCCCGGCTGGTGATGGCCCCAGGAC
 1027▶ GluAsnTyrArgPheHisAlaIleAsnGlyTyrIleMetAspThrLeuProGlyLeuValMetAlaGlnAsp

KpnI

PmlI

3169 CAGCGCATCCGCTGGTACCTGCTGAGCATGGGCAGCAACGAGAACATCCACAGCATCCACTTCAGCGGCCAC
 1051▶ GlnArgIleArgTrpTyrLeuLeuSerMetGlySerAsnGluAsnIleHisSerIleHisPheSerGlyHis
 3241 GTGTTACCGTGGCGAAGAAGGAGGAGTACAAGATGGCCCTGTACAACCTGTACCCCGGCGTGTTCGAGACC
 1075▶ ValPheThrValArgLysLysGluGluTyrLysMetAlaLeuTyrAsnLeuTyrProGlyValPheGluThr
 3313 GTGGAGATGCTGCCCAGCAAGGCCGGCATCTGGCGCGTGGAGTGCCTGATCGGCGAGCACCTGCACGCCGGC
 1099▶ ValGluMetLeuProSerLysAlaGlyIleTrpArgValGluCysLeuIleGlyGluHisLeuHisAlaGly
 3385 ATGAGCACCCCTGTTCTCTGCTGTACAGCAACAAGTGCAGACCCCCCTGGGCATGGCCAGCGGCCACATCCGC
 1123▶ MetSerThrLeuPheLeuValTyrSerAsnLysCysGlnThrProLeuGlyMetAlaSerGlyHisIleArg

Apal

3457 GACTTCCAGATCACCGCCAGCGGCCAGTACGGCCAGTGGGCCCCCAAGCTGGCCCGCTGCACTACAGCGGC
 1147▶ AspPheGlnIleThrAlaSerGlyGlnTyrGlyGlnTrpAlaProLysLeuAlaArgLeuHisTyrSerGly
 3529 AGCATCAACGCCTGGAGCACCAAGGAGCCCTTCAGCTGGATCAAGGTGGACCTGCTGGCCCCCATGATCATC
 1171▶ SerIleAsnAlaTrpSerThrLysGluProPheSerTrpIleLysValAspLeuLeuAlaProMetIleIle
 3601 CACGGCATCAAGACCCAGGGCGCCCGCCAGAAGTTCAGCAGCCTGTACATCAGCCAGTTCATCATCATGTAC
 1195▶ HisGlyIleLysThrGlnGlyAlaArgGlnLysPheSerSerLeuTyrIleSerGlnPheIleIleMetTyr
 3673 AGCCTGGACGGCAAGAAGTGGCAGACCTACCGCGGCAACAGCACCGGCACCCTGATGGTGTCTCTCGGCAAC
 1219▶ SerLeuAspGlyLysLysTrpGlnThrTyrArgGlyAsnSerThrGlyThrLeuMetValPhePheGlyAsn

(SmaI/EcoRV)

3745 GTGGACAGCAGCGGCATCAAGCACAACATCTTCAACCCCCCATCATCGCCCCCTACATCCGCTGCACCCC
 1243▶ ValAspSerSerGlyIleLysHisAsnIlePheAsnProProIleIleAlaArgTyrIleArgLeuHisPro
 3817 ACCCACTACAGCATCCCGACGACCCCTGCGCATGGAGCTGATGGGCTGCGACCTGAACAGCTGCAGCATGCCC
 1267▶ ThrHisTyrSerIleArgSerThrLeuArgMetGluLeuMetGlyCysAspLeuAsnSerCysSerMetPro
 3889 CTGGGCATGGAGAGCAAGGCCATCAGCGACGCCCCAGATCACCGCCAGCAGCTACTTCAACCAACATGTTCCGCC
 1291▶ LeuGlyMetGluSerLysAlaIleSerAspAlaGlnIleThrAlaSerSerTyrPheThrAsnMetPheAla
 3961 ACCTGGAGCCCCAGCAAGGCCCGCTGCACCTGCAGGGCGCGCAGCAACGCCTGGCGCCCCCAGGTGAACAAC
 1315▶ ThrTrpSerProSerLysAlaArgLeuHisLeuGlnGlyArgSerAsnAlaTrpArgProGlnValAsnAsn

BstEII

4033 CCCAAGGAGTGGCTGCAGGTGGACTTCCAGAAGACCATGAAGGTGACCGGCGTGACCACCCAGGGCGTGAAG
 1339▶ ProLysGluTrpLeuGlnValAspPheGlnLysThrMetLysValThrGlyValThrThrGlnGlyValLys
 4105 AGCCTGCTGACCAGCATGTACGTGAAGGAGTTCCTGATCAGCAGCAGCCAGGACGGCCACCACTGGACCCCTG
 1363▶ SerLeuLeuThrSerMetTyrValLysGluPheLeuIleSerSerSerGlnAspGlyHisGlnTrpThrLeu
 4177 TTCTTCCAGAACGGCAAGGTGAAGGTGTTCCAGGGCAACAGGACAGCTTCACCCCCCTGGTGAACAGCCTG
 1387▶ PhePheGlnAsnGlyLysValLysValPheGlnGlyAsnGlnAspSerPheThrProValValAsnSerLeu
 4249 GACCCCCCCCCCTGCTGACCCGCTACCTGCGCATCCACCCCCAGAGCTGGGTGCACAGATCGCCCTGCGCATG
 1411▶ AspProProLeuLeuThrArgTyrLeuArgIleHisProGlnSerTrpValHisGlnIleAlaLeuArgMet

SmaI

HindIII

AM18F1

AM8R4

AM18F-R2

30151

AM18BR2

 $5'P \quad 3'OH$

BstXI

Hirdin

GCCTATAGGAGAGATCGACTACGACGACACCATCAGCGTGAAGCTTTAC
CGCTGCTCTCTCTAGCTGATGCTGCTGTGTAGTGTGACCTTGAATG
AM8R1

AM18P1

FIG. 8

EcoRI NheI

1 TAGAATTCCTAGGCTAGCATGCAGATCGAGCCTCAGCACCTTGTCTTCCCTGTGCCCTCCTCGGCTTTCTGGCTTC
1 MetGlnIleGluLeuSerThrCysPhePheLeuCysLeuLeuArgPheCysPhe

73 AGCGCCCACCGCCCGCTACTACCCTGGGCGCCCTGGAGCTCAGCTGGGACTACATGCAGAGCGACCTGGGCGAG
19 SerAlaThrArgArgTyrTyrLeuGlyAlaValGluLeuSerTrpAspTyrMetGlnSerAspLeuGlyGlu

145 CTGCCCCGTGGACGCCCGCTTCCCCCCCCCCGCGTGCCCAAGAGCTTCCCCCTCAACACCAGCGTGGTGTACAAG
43 LeuProValAspAlaArgPheProProArgValProLysSerPheProPheAsnThrSerValValTyrLys

117 AAGACCCTGTTTCGTGGAGTTCACCGACCACCTTTCCAACATCGCCAAAGCCCCGCCCCCCTGGATGGGCGCTG
67 LysThrLeuPheValGluPheThrAspHisLeuPheAsnIleAlaLysProArgProProTrpMetGlyLeu

Apal MscI

289 CTGGGCCCCACCATTCCAGGCCGAGGTGTACGACACCGTGGTGATCACCCTGAAGAACATGGCCAGCCACCCC
91 LeuGlyProThrIleGlnAlaGluValTyrAspThrValValIleThrLeuLysAsnMetAlaSerHisPro

361 GTGAGCCTGCACGCCGTGGGCGTGAGCTACTGGAAGGCCAGCGAGGGCGCCGAGTAGCAGCAGCAGACCAGC
115 ValSerLeuHisAlaValGlyValSerTyrTrpLysAlaSerGluGlyAlaGluTyrAspAspGlnThrSer

433 CAGCGCGAGAAGGAGGACGACAAGGTGTTCCCCGCGGGCAGCCACACCTACGTGTGGCAGGTGCTGAAGGAG
139 GlnArgGluLysGluAspAspLysValPheProGlyGlySerHisThrTyrValTrpGlnValLeuLysGlu

MscI PmlI

505 AACGGCCCCATCGCCAGCGAACCCCTGTGCCTGCCTACAGCTACCTGAGCCACGTGGACCTGGTGAAGGAC
163 AsnGlyProMetAlaSerAspProLeuCysLeuThrTyrSerTyrLeuSerHisValAspLeuValLysAsp

MscI

577 CTGAACAGCGGCCTGATCGGCGCCCTGCTGGTGTGCCGCGAGGGCAGCCTGGCCAAGGAGAAGACCCAGACC
187 LeuAsnSerGlyLeuIleGlyAlaLeuLeuValCysArgGluGlySerLeuAlaLysGluLysThrGlnThr

649 CTGCACAAGTTCATCCTGCTGTTTCGCCGTGTTTCGACGAGGGCAAGAGCTGGCACAGCGAGACCAAAGAACAGC
211 LeuHisLysPheIleLeuLeuPheAlaValPheAspGluGlyLysSerTrpHisSerGluThrLysAsnSer

721 CTGATGCAGGACCGCGACGCCGCCAGCGCCCCGCGCTGGCCCCAAGATGCACACCGTGAACGGCTACGTGAAC
235 LeuMetGlnAspArgAspAlaAlaSerAlaArgAlaTrpProLysMetHisThrValAsnGlyTyrValAsn

PmlI

793 CGCAGCCTGCCCCGGCCTGATCGGCTGCCACCGCAAGAGCGTGTA TGGCACGTGATCGGCATGGGCACCCACC
259 ArgSerLeuProGlyLeuIleGlyCysHisArgLysSerValTyrTrpHisValIleGlyMetGlyThrThr

865 CCCGAGGTGCACAGCATCTTCTCTGGAGGGCCACACCTTCTCTGGTGGCGCAACCACCGCCAGGCCAGCCTGGAG
283 ProGluValHisSerIlePheLeuGluGlyHisThrPheLeuValArgAsnHisArgGlnAlaSerLeuGlu

937 ATCAGCCCCATCACCTTCTGTACCGCCCCAGACCCTGCTGATGGACCTGGGCGAGTTCCTGCTGTTTTCTGCCAC
307 IleSerProIleThrPheLeuThrAlaGlnThrLeuLeuMetAspLeuGlyGlnPheLeuLeuPheCysHis

1009 ATCAGCAGCCACCAGCAGCAGCGGCATGGAGGCCCTACGTGAAGGTGGACAGCTGCCCCGAGGAGCCCCAGCTG
331 IleSerSerHisGlnHisAspGlyMetGluAlaTyrValLysValAspSerCysProGluGluProGlnLeu

1081 CGCATGAAGAACAACGAGGAGGCCGAGGACTACGACGACGACCTGACCGACAGCGAGATGGACGTGGTGGCG
355 ArgMetLysAsnAsnGluGluAlaGluAspTyrAspAspAspLeuThrAspSerGluMetAspValValArg

(BglII/BamHI)

1153 TTCGACGACGACAACAGCCCCAGCTTCATCCAGATCCCGACGGTGGCCAAGAAGCACCCCCAGACCTGGGTG
379 PheAspAspAspAsnSerProSerPheIleGlnIleArgSerValAlaLysLysHisProLysThrTrpVal

1225 CACTACATCGCCGCGGAGGAGGAGGACTGGGACTACGCCCCCCTGGTGTCTGGCCCCCGACGACCCAGCTAC
403 HisTyrIleAlaAlaGluGluGluAspTrpAspTyrAlaProLeuValLeuAlaProAspAspArgSerTyr

EagI

1297 AAGAGCCAGTACCTGAACAACGGCCCCCAGCGCATCGGCCCAAGTACAAGAAGGTGGCGTTTCATGGCCTAC
427 LysSerGlnTyrLeuAsnAsnGlyProGlnArgIleGlyArgLysTyrLysLysValArgPheMetAlaTyr

Apal

1441 JAGGTGGGGGACACCCCTGCTGATCATCTTCAAGAACCAGGCCAGCCCCCCTACAACATCTACCCCCACGGC
 475> GluValGlyAspThrLeuLeuIleIlePheLysAsnGlnAlaSerArgProTyrAsnIleTyrProHisGly
 1513 ATCACCCAGCTGCGCCCCCTGTACAGCCGCGCCCTGCCCAAGGGCGTGAAGCACCTGAAGGACTTCCCCATC
 499> IleThrAspValArgProLeuTyrSerArgArgLeuProLysGlyValLysHisLeuLysAspPheProIle

BglII

1585 CTGCCCCGGCGAGATCTTCAAGTACAAGTGGACCCTGACCCTGGAGGACGGCCCCACCAAGAGCGACCCCCGC
 523> LeuProGlyGluIlePheLysTyrLysTrpThrValThrValGluAspGlyProThrLysSerAspProArg
 1657 TGCCTGACCCCGCTACTACAGCAGCTTCGTGAACATGGAGCGCGACCTGGCCAGCGGCTGATCGGCCCCCTG
 547> CysLeuThrArgTyrTyrSerSerPheValAsnMetGluArgAspLeuAlaSerGlyLeuIleGlyProLeu
 1729 CTGATCTGCTACAAGGAGAGCGTGGACCAGCGCGGCAACCAGATCATGAGCGACAAGCGCAACCTGATCCTG
 571> LeuIleCysTyrLysGluSerValAspGlnArgGlyAsnGlnIleMetSerAspLysArgAsnValIleLeu

KpnI

1801 TTCAGCGTGTTCGACGAGAACCACAGCTCGTACCTGACCCAGAACATCCAGCGCTTCCTGCCCAACCCCGCC
 595> PheSerValPheAspGluAsnArgSerTrpTyrLeuThrGluAsnIleGlnArgPheLeuProAsnProAla
 1873 GCGGTGCAGCTGGAGGACCCCGAGTTCCAGGCCAGCAACATCATGCACAGCATCAACGGCTACGTGTTTCGAC
 619> GlyValGlnLeuGluAspProGluPheGlnAlaSerAsnIleMetHisSerIleAspGlyTyrValPheAsp
 1945 ACCCTCCAGCTGAGCGTGTGCTGACAGAGGTGGCCTACTGGTACATCCTGAGCATCGGCGCCAGACCGAC
 643> SerLeuGlnLeuSerValCysLeuHisGluValAlaTyrTrpTyrIleLeuSerIleGlyAlaGlnThrAsp
 2017 TTCCTGAGCGTGTTCCTCAGCGCTACACCTTCAAGCACAAGATGGTGTACGAGGACACCCTGACCCTGTTC
 667> PheLeuSerValPhePheSerGlyTyrThrPheLysHisLysMetValTyrGluAspThrLeuThrLeuPhe

BamHI

2089 CCCTTCAGCGGCGAGACCGTGTTCATGAGCATGGAGAACCCTGGCCTGTGGATCCTGGGCTGCCACAACAGC
 691> ProPheSerGlyGluThrValPheMetSerMetGluAsnProGlyLeuTrpIleLeuGlyCysHisAsnSer
 2161 GACTTCCGCAACCGCGGCATGACCGCCCTGCTGAAGGTGAGCAGCTGCGACAAGAACACCGGCGACTACTAC
 715> AspPheArgAsnArgGlyMetThrAlaLeuLeuLysValSerSerCysAspLysAsnThrGlyAspTyrTyr
 2233 GAGGACAGCTACGAGGACATCAGCGCCTACCTGCTGAGCAAGAACAACGCCATCGAGCCCCGAGGCGCAGG
 739> GluAspSerTyrGluAspIleSerAlaTyrLeuLeuSerLysAsnAsnAlaIleGluProArgArgArgArg

BstXI

2305 GCGGAGATCACCCGCACCACCTGCAGAGCGACCCAGGAGGAGATCGACTACGACGACACCATCAGCGTGGAG
 763> ArgGluIleThrArgThrThrLeuGlnSerAspGlnGluGluIleAspTyrAspAspThrIleSerValGlu
 2377 ATGAAGAAGGAGGACTTCGACATCTACGACGAGGACGAGAACCAGAGCCCCCGAGCTTCCAGAAGAAGACC
 787> MetLysLysGluAspPheAspIleTyrAspGluAspGluAsnGlnSerProArgSerPheGlnLysLysThr

PmlI

2449 CGCCACTACTTCATCGCGCCCGTGGAGCGCCTGTGGGACTACGGCATGAGCAGCAGCCCCACCGTGTCTGCGC
 811> ArgHisTyrPheIleAlaAlaValGluArgLeuTrpAspTyrGlyMetSerSerSerProHisValLeuArg
 2521 AACCGCGCCCAGAGCGGCGAGCGTGGCCCAAGTTCAAGAAGGTGGTGTCCAGGAGTTCACCGACGGCAGCTTC
 835> AsnArgAlaGlnSerGlySerValProGlnPheLysLysValValPheGlnGluPheThrAspGlySerPhe

Apal

2593 ACCCAGCCCCCTGTACCGCGCGGAGCTGAACGAGCACCTGGGCTCTGGGCCCCCTACATCCGCGCCGAGGTG
 859> ThrGlnProLeuTyrArgGlyGluLeuAsnGluHisLeuGlyLeuLeuGlyProTyrIleArgAlaGluVal

BstEII

2665 CAGGACAACATCATGGTGACCTTCGGCAACCAGGCCAGCCGCCCTACAGCTTCTACAGCAGCCTGATCAGC
 883> GluAspAsnIleMetValThrPheArgAsnGlnAlaSerArgProTyrSerPheTyrSerSerLeuIleSer
 2737 TACGAGGAGGACCGAGCGCCAGGGCGCCGAGCCCCGCAAGAAGTTCGTGAAGCCCAACGAGACCAAGACCTAC
 907> TyrGluGluAspGlnArgGlnGlyAlaGluProArgLysAsnPheValLysProAsnGluThrLysThrTyr

2381 TACGTGGACCTGGAGAAGGACGTGCACAGCGGCCTGATCGGCCCCCTGCTGGTGTGCCACACCAACACCCCTG
 955▶ AspValAspLeuGluLysAspValHisSerGlyLeuIleGlyProLeuLeuValCysHisThrAsnThrLeu
 EagI BstEII
 2953 AACCCCGCCCCACGGCCGCCAGGTGACCCCTGCAGGAGTTCCGCCCTGTTCTTCACCATCTTCGACGAGACCAAG
 979▶ AsnProAlaHisGlyArgGlnValThrValGlnGluPheAlaLeuPhePheThrIlePheAspGluThrLys
 3025 AGCTGGTACTTCCACCGAGAACATGGAGCGCAACTGCCGCGCCCCCTGCAACATCCAGATGGAGGACCCACCC
 1003▶ SerTrpTyrPheThrGluAsnMetGluArgAsnCysArgAlaProCysAsnIleGlnMetGluAspProThr
 3097 TTCAAGGAGAACTACCGCTTCCACGCCATCAACGGCTACATCATGGACACCCCTGCCCGGCCTGGTGATGGCC
 1027▶ PheLysGluAsnTyrArgPheHisAlaIleAsnGlyTyrIleMetAspThrLeuProGlyLeuValMetAla
 KpnI
 3169 CAGGACCAGCGCATCCGCTGGTACCTGCTGAGCATGGGCAGCAACGAGAACATCCACAGCATCCACTTCAGC
 1051▶ GlnAspGlnArgIleArgTrpTyrLeuLeuSerMetGlySerAsnGluAsnIleHisSerIleHisPheSer
 PmlI
 3241 GGCCACGTGTTCCACCGTGCGCAAGAAGGAGGAGTACAAGATGGCCCTGTACAACCTGTACCCCGGCGTGTTTC
 1075▶ GlyHisValPheThrValArgLysLysGluGluTyrLysMetAlaLeuTyrAsnLeuTyrProGlyValPhe
 3313 GAGACCGTGGAGATGCTGCCACGCAAGCCCGCATCTGGCGCGTGGAGTGCCTGATCGGCGAGCACCTGCAC
 1099▶ GluThrValGluMetLeuProSerLysAlaGlyIleTrpArgValGluCysLeuIleGlyGluHisLeuHis
 3385 GCGGCGATGAGCACCCCTGTTCTGCTGTACAGCAACAAGTGCACAGCCCCCTGGGGATGGCCAGCGGGCCAC
 1123▶ AlaGlyMetSerThrLeuPheLeuValTyrSerAsnLysCysGlnThrProLeuGlyMetAlaSerGlyHis
 ApaI
 3457 ATCCGCGACTTCCAGATCACCGCCAGCGGCCAGTACGGCCAGTGGGCCCCCAAGCTGGCCCGCCTGCACTAC
 1147▶ IleArgAspPheGlnIleThrAlaSerGlyGlnTyrGlyGlnTrpAlaProLysLeuAlaArgLeuHisTyr
 3529 AGCGGCAGCATCAACGCCTGGAGCACCAAGGAGCCCTTCAGCTGGATCAAGGTGGACCTGCTGGCCCCCATG
 1171▶ SerGlySerIleAsnAlaTrpSerThrLysGluProPheSerTrpIleLysValAspLeuLeuAlaProMet
 3601 ATCATCCACGGCATCAAGACCCAGGGCGCCCGCCAGAAGTTCAGCAGCCTGTACATCAGCCAGTTCATCATC
 1195▶ IleIleHisGlyIleLysThrGlnGlyAlaArgGlnLysPheSerSerLeuTyrIleSerGlnPheIleIle
 3673 ATGTACAGCCTGGACGGCAAGAAGTGGCAGACCTACCGCGGCAACAGCACCGGCACCCTGATGGTGTCTCTC
 1219▶ MetTyrSerLeuAspGlyLysLysTrpGlnThrTyrArgGlyAsnSerThrGlyThrLeuMetValPhePhe
 (SmaI/EcoRV)
 3745 GGCAACGTGGACAGCAGCGGCATCAAGCACAAACATCTTCAACCCCCCATCATCGCCCCGTACATCCGCCCTG
 1243▶ GlyAsnValAspSerSerGlyIleLysHisAsnIlePheAsnProProIleIleAlaArgTyrIleArgLeu
 3817 CACCCCAACCCACTACAGCATCCGCAGCACCCCTGCGCATGGAGCTGATGGGCTGCGACCTGAACAGCTGCAGC
 1267▶ HisProThrHisTyrSerIleArgSerThrLeuArgMetGluLeuMetGlyCysAspLeuAsnSerCysSer
 3889 ATGCCCCCTGGGCATGGAGAGCAAGGCCATCAGCGACGCCCAGATCACCGCCAGCAGCTACTTCACCAACATG
 1291▶ MetProLeuGlyMetGluSerLysAlaIleSerAspAlaGlnIleThrAlaSerSerTyrPheThrAsnMet
 3961 TTCGCCACCTGGAGCCCCAGCAAGGCCCGCCTGCACCTGCAGGGCCGCGAGCAACGCCTGGCGCCCCCAGGTG
 1315▶ PheAlaThrTrpSerProSerLysAlaArgLeuHisLeuGlnGlyArgSerAsnAlaTrpArgProGlnVal
 BstEII
 4033 AACAAACCCCAAGGAGTGGCTCCAGGTGGACTTCCAGAAGACCATGAAGGTGACCGGCGTGACCACCCAGGGC
 1339▶ AsnAsnProLysGluTrpLeuGlnValAspPheGlnLysThrMetLysValThrGlyValThrThrGlnGly
 4105 GTGAAGAGCCTGCTGACCAGCATGTACGTGAAGGAGTTCTCTGATCAGCAGCAGCCAGGACGSCCACCAGTGG
 1363▶ ValLysSerLeuLeuThrSerMetTyrValLysGluPheLeuIleSerSerSerGlnAspGlyHisGlnTrp
 4177 ACCCTGTTCTTCCAGAACGGCAAGGTGAAGGTGTTCCAGGGCAACAGGACAGCTTCACCCCGCTGGTGAAC
 1387▶ ThrLeuPhePheGlnAsnGlyLysValLysValPheGlnGlyAsnGlnAspSerPheThrProValValAsn
 4249 AGCCTGGACCCCCCTGCTGACCCGCTACCTGCGCATCCACCCCGAGAGCTGGGTGCACCAGATCGCCCTG
 1411▶ SerLeuAspProProLeuLeuThrArgTyrLeuArgIleHisProGlnSerTrpValHisGlnIleAlaLeu
 SmaI HindIII

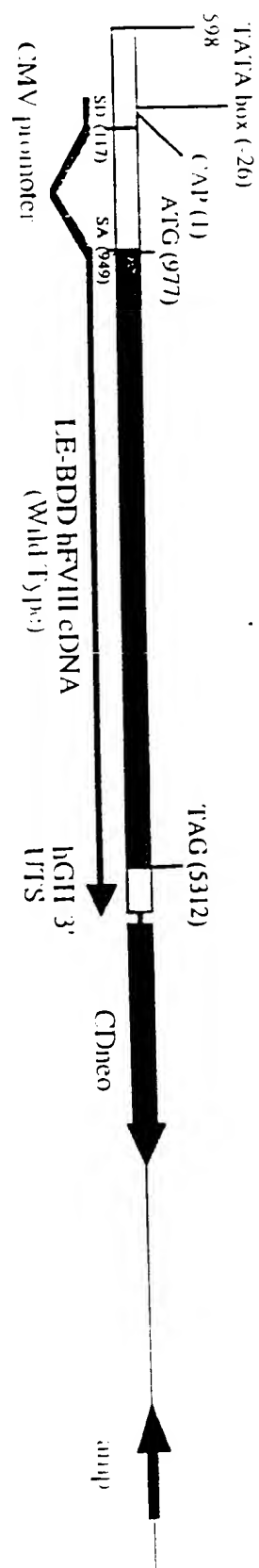


FIG. 10

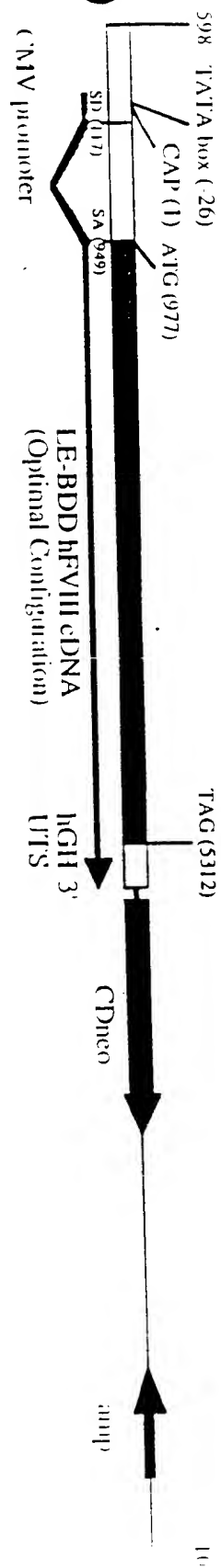


FIG. 11

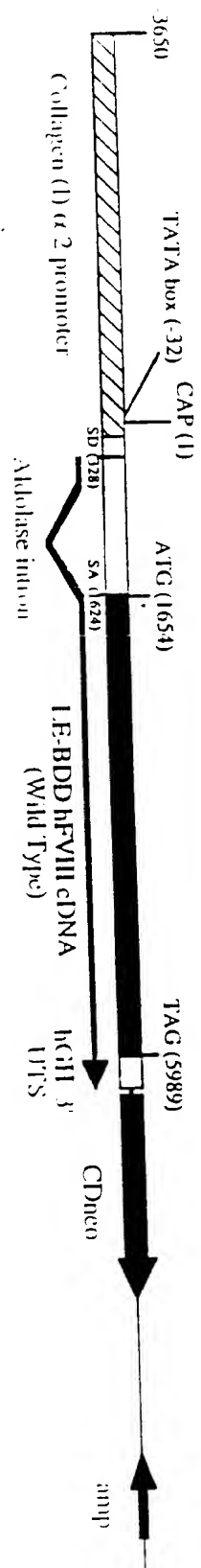


FIG. 12

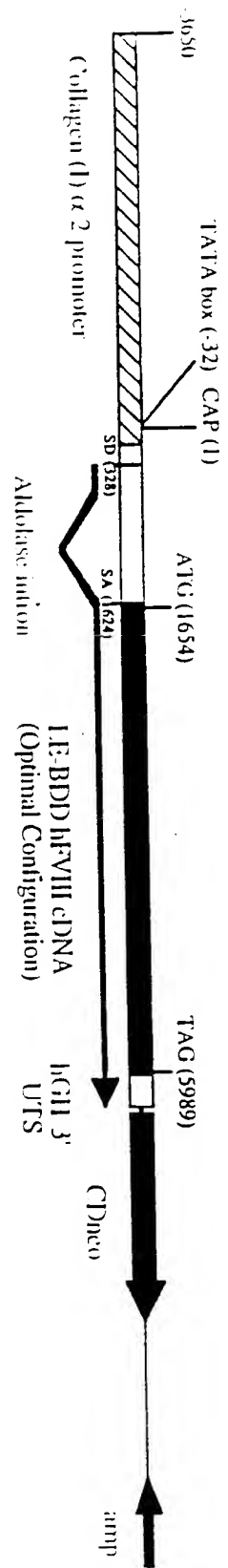


FIG. 13